RAW SEQUENCE LISTING
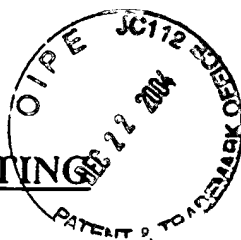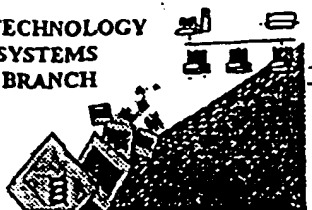## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/696,488
Source: TWO
Date Processed by STIC: 10-13-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10/696,488

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics / Wrapped Aminos   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .): this will prevent "wrapping."

2 ___ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering   The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length   Sequence(s)___contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6 ___ PatentIn 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES)   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X_(insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES " response to include the skipped sequences

8 ___ Skipped Sequences (NEW RULES)   Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ___ Invalid <213> Response   Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>   Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

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IFWO

RAW SEQUENCE LISTING   DATE: 10/13/2004
PATENT APPLICATION: US/10/696,488 TIME: 10:12:28

Input Set : A:\sequence listing-1-02.txt
Output Set: N:\CRF4\10132004\J696488.raw

```
 4 <110> APPLICANT: Cuenoud, Bernard
 5         Altmann, Karl-Heinz
 6         Martin, Pierre
 7         Moser, Heinz Ernst
 9 <120> TITLE OF INVENTION: 2'-Substituted Nucleosides and Oligonucleotide Derivatives
11 <130> FILE REFERENCE: 4-20890B/C1
```
C--> 13 `<140> CURRENT APPLICATION NUMBER: US/10/696,488`
C--> 14 `<141> CURRENT FILING DATE: 2003-10-29`
```
16 <150> PRIOR APPLICATION NUMBER: 09/194,844
17 <151> PRIOR FILING DATE: 1999-05-14
19 <150> PRIOR APPLICATION NUMBER: PCT/EP97/02738
20 <151> PRIOR FILING DATE: 1998-05-27
22 <150> PRIOR APPLICATION NUMBER: Switzerland 1432/96
23 <151> PRIOR FILING DATE: 1996-06-06
```

<160> - please insert mandatory numeric identifier <160> with response. *(pg. 1-4)*

ERRORED SEQUENCES

```
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 20
27 <212> TYPE: RNA
28 <213> ORGANISM: Homo sapiens
```
E--> 0 `<160> NUMBER OF SEQ ID NOS:`
W--> 29 `<400> SEQUENCE: 1`
```
30 aaugcauguc acaggcggga    20
173 <210> SEQ ID NO: 14
174 <211> LENGTH: 13
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
```
Pls see item #11 on error summary sheet.

W--> 177 `<220> FEATURE:`
W--> 178 `<221> NAME/KEY: 2'-substituted sugar`
Please explain source of genetic material.
```
179 <222> LOCATION: 4, 6, 12
180 <223> OTHER INFORMATION: Locations 4, 6, 12 = 2'-substituted sugar
```
W--> 181 `<400> SEQUENCE: 14`
E--> 182 `aggtgtccgc atc    13`

Invalid Response

Type of errors shown exist throughout Sequence Listing. Please check subsequent sequences for similar errors

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```
<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence         Sequence
<220>
<221> phosphorothioate backbone
<222> 1-20
<221> 2'-substituted sugar
<222> 1-5 and 15-19
<223> Locations 1-20 = phosphorothioate backbone
      Locations 1-5 and 15-19 = 2'-substituted sugar
<400> 22
tcccgcctgt gacatgcatt                    20
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/696,488

DATE: 10/13/2004
TIME: 10:12:29

Input Set : A:\sequence listing-1-02.txt
Output Set: N:\CRF4\10132004\J696488.raw

```
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:282 E: Numeric Field Identifier Missing, <160> is required.
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:40 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:283 W: Missing Blank Line separator, <220> field identifier
L:48 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:58 M:283 W: Missing Blank Line separator, <220> field identifier
L:59 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:73 M:283 W: Missing Blank Line separator, <400> field identifier
L:80 M:283 W: Missing Blank Line separator, <220> field identifier
L:81 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:84 M:283 W: Missing Blank Line separator, <400> field identifier
L:91 M:283 W: Missing Blank Line separator, <220> field identifier
L:92 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:94 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:98 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:98 M:283 W: Missing Blank Line separator, <400> field identifier
L:105 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:108 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:112 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
L:119 M:283 W: Missing Blank Line separator, <220> field identifier
L:120 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:122 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:126 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:137 M:283 W: Missing Blank Line separator, <400> field identifier
L:144 M:283 W: Missing Blank Line separator, <220> field identifier
L:145 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:148 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:283 W: Missing Blank Line separator, <220> field identifier
L:156 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:159 M:283 W: Missing Blank Line separator, <400> field identifier
L:166 M:283 W: Missing Blank Line separator, <220> field identifier
L:167 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:170 M:283 W: Missing Blank Line separator, <400> field identifier
L:177 M:283 W: Missing Blank Line separator, <220> field identifier
L:178 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
```

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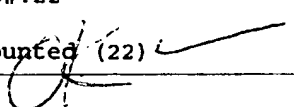VERIFICATION SUMMARY   DATE: 10/13/2004
PATENT APPLICATION: US/10/696,488   TIME: 10:12:29

Input Set : A:\sequence listing-1-02.txt
Output Set: N:\CRF4\10132004\J696488.raw

L:181 M:283 W: Missing Blank Line separator, <400> field identifier
L:182 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:188 M:283 W: Missing Blank Line separator, <220> field identifier
L:189 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:192 M:283 W: Missing Blank Line separator, <400> field identifier
L:199 M:283 W: Missing Blank Line separator, <220> field identifier
L:200 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:210 M:283 W: Missing Blank Line separator, <220> field identifier
L:211 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:214 M:283 W: Missing Blank Line separator, <400> field identifier
L:221 M:283 W: Missing Blank Line separator, <220> field identifier
L:222 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:224 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:228 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18
L:228 M:283 W: Missing Blank Line separator, <400> field identifier
L:235 M:283 W: Missing Blank Line separator, <220> field identifier
L:236 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:238 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:242 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19
L:242 M:283 W: Missing Blank Line separator, <400> field identifier
L:249 M:283 W: Missing Blank Line separator, <220> field identifier
L:250 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:252 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:256 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20
L:256 M:283 W: Missing Blank Line separator, <400> field identifier
L:263 M:283 W: Missing Blank Line separator, <220> field identifier
L:264 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:266 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:270 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21
L:270 M:283 W: Missing Blank Line separator, <400> field identifier
L:276 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:277 M:283 W: Missing Blank Line separator, <220> field identifier
L:278 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:280 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:284 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22
L:284 M:283 W: Missing Blank Line separator, <400> field identifier
L:0 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (22)

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